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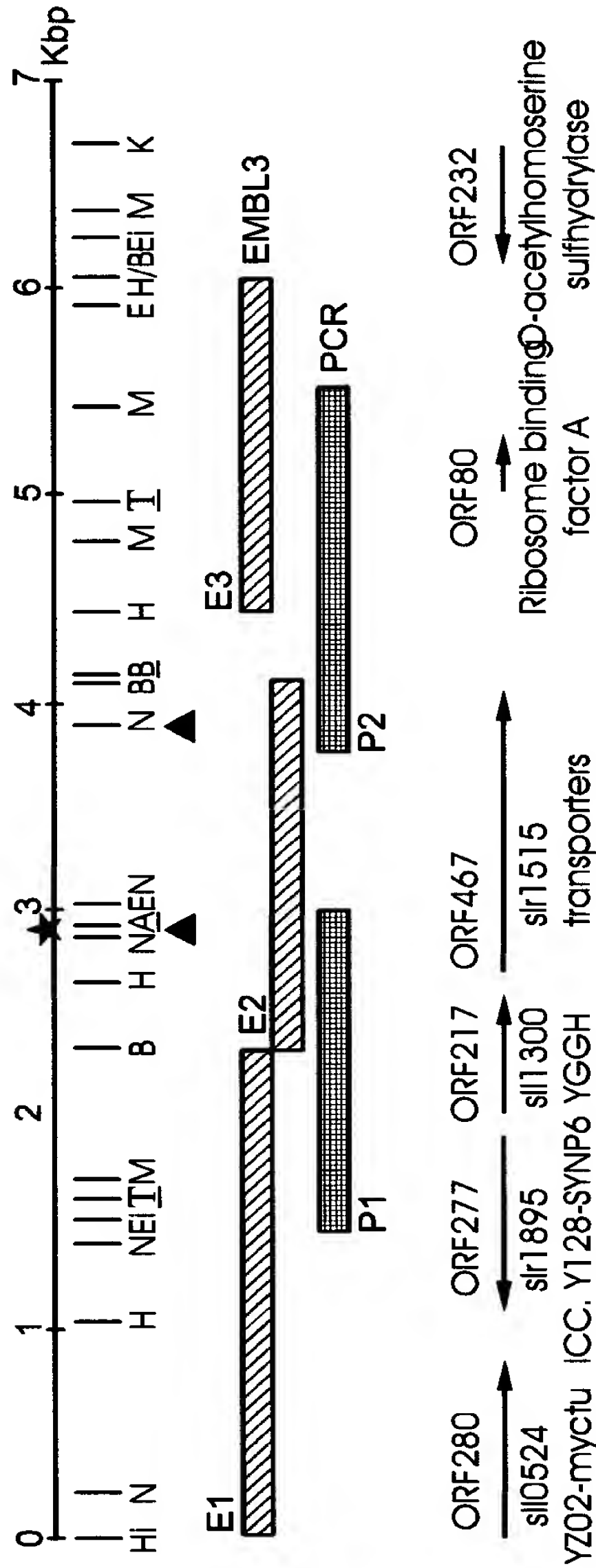
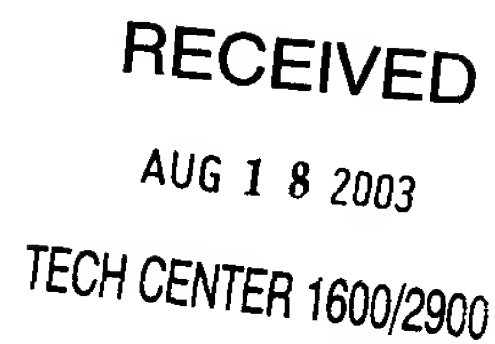


Fig. 1



ICTB : 1 ATGACTGTCTGGCAAACTCTGACCTTTTGCCCATTTACC AACCCAACAGTGGGCCACAGC 60 (SEQ ID NO:2)

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SLR : 13 ATCTCTATCTGGCGATCGCTGATGTTTGGCGGTTTTTC CCCCAGGAATGGGCCGGGC 72 (SEQ ID NO:4)

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ICTB : 61  AGTTTCTTGCAATCGGCTGTTTGGCAGCCTGC-GAGCTTGGCGGCCCTCCAGCCAGCTGT 119
          ||| | | ||||| || | ||| | | ||| |||| | || | ||| |
SLR  : 73  AGTGTGCTCCATCGTTTGGTGGGCTGGGGACAGAG-TTGGATACAGGCTAGTGTGCTCTG 131

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IICTB : 120  GGTGGTCTGAGGCACTGGGT--GGCTTCTTGCTTGCTGCTACGGTTCGGCTCCG 177
          |      |      |      |      |      |      |      |      |
SLR    : 132  GCCCAGCTTCGAGGCATGGGTACGGCT-CTAG-TGGCAATAATTTTATTGCGGCTCCC 189

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ICTB : 178 TTTGTGCCAGTTCGCCCTAGGTTGGGCTAGCCGCGATCGCG-GCCTATTGGGCCCT 236
      ||      |||      ||      |||      |      |||      |||      |||
SLR  : 190 TTCACCTCCACCACCATGTTGGGCATTTTAT-GCTGCTCTGTGGAGCCTTTTGGGCTCT 248

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ICTB : 237 GCTCTGGCTGACAGATATCGATCTGCGGCAAGCA---ACCCCCATTCACCTGGCTGCT 293
 ||| | | ||| | | | | | | | | | | | | | | | |
 SLR : 249 GCTGACCTTTGCTGAT--CAACCAG-GGAAGGGTTTGACTCCCATCCATGTTTATGTTT 305

ICTB : 294 GCTCTACTGGGCGTCGATGCCCTAGCCCTACGCGACTCTCACCCGTACCGCTGCAGCTTT 353
||||| | | | | | | | | | | | | | |
SSLR : 306 TGCCTACTGGTGCAATTTCGGCGATCGCCGTGGGATTTTCTCCGGTAATAAATGGCGCGCGC 365

ICTB : 354 AGTTGGGCTAGCCAAACTGAC-GCTC-TACCTGTGGTTTTTGCCCTAGCGGCTCGGGTT 411
||| ||| ||| | ||| | ||| ||| | ||| ||| |||
SLR : 366 GTCGGGGTTAGCGAAATTAAACAGCTAATTTATGCTCTGTTTCTAC--TGGCGGGCGAGGTTA 423

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ICTB : 412  CTCGGCAATCCCCGCTGCGATCGCTGCTGTTCTCGGTCGTGATCACATCGCTTT 470
      | | | | | | | | | | | | | | | | | | | |
SLR : 424  TTGCAAAACAAACAATGGTTGAAC-CGGTTAGTAACCGTTGTTTACTGGTAGGGCTATT 482

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Fig. 2a

Fig. 2a

Fig. 2b

Fig. 2c

Fig. 2

ICTB : 471	TGTCAGTGTCTACGGCCTCAACCAATGGATCTACGGCGTTGAAGAGCTGGCGACTTGGGT	530
SLR : 483	GGTGGGAGTTACGGTCTCGGACACACAGGTGGACGGGTAGAACAGTTAGCCACTTGGAA	542
ICTB : 531	GGATCGCAACTCGGTTGCCGACTTCACCTCACGGGTTTACAGCTATCTGGGCAACCCCAA	590
SLR : 543	TGACCCCACTCTACCTTGCCCAAGCCACTAGGGTATATAGCTTTTTAGGTAATCCCAA	602
ICTB : 591	CCTGCTGGCTGCTTAICTGGTGCCGACGACTGCCCTTTT-CTGCAGCAGCGATCGGGGTGT	649
SLR : 603	TCTCTTGGCGGCTTACCTGGTGCCCATGACGGGTTTGAGCTTGAGT-GCCCTGGTGGTAT	661
ICTB : 650	GGCGCGGCTGGCTCCCAAGCTGCTGGCGATCG-CTGCGACAGGTGCGAGCAGCTTATGT	708
SLR : 662	GGCGACGGTGGTGGCCCAAACTGCTGG-GAGCAACCATGGTGATTGTTAACCTACTCTGT	720
ICTB : 709	CTGATCCTCACCTACAGTCGCGGTGGCTGGCTGGGTTTGTGCGCCATGATTTTGTCTGTG	768
SLR : 721	CTCTTTTACCAGAGCCGGGGGGTGGCTAGCAGTGCTGGCCCTGGGAGCTACCTTC	780
ICTB : 769	GGGTTATTAGGGCTCTACTGGTTTCAACCCCGTCTACCCGCACCCCTGGCGACGCTGGCTA	828
SLR : 781	CTGGCCCCTTGTACTTCTGTGTGTTACCCCAATTACCCAAATTTTGGCAACGGTGGTCT	840
ICTB : 829	TTCCCAGTCGTATTGGGTGGACTAGTCGCGGTGCTCTT-GGTGCGGTGCTTGGACT---	884
SLR : 841	TTGCCCCCTGGC---GATCGCC--GTGGCGGTTATATTAGGTGGGGGAGCGTTGATTGCG	894
ICTB : 885	-TG-AGCCGTTGCGCGTGCAGCTGTTGAGCATCTTTGTGGGCGTGAAGACAGCAGCAAC	942
SLR : 895	GTGGAACCGATTCCGACTCAGGGCCATGAGCATTTTTCCTGGCGGGAAGACAGCAGTAAT	954

Fig. 2b

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ICTB : 943   AACTTCCGGATCAATGTCTGGCTGCGGTGCTGCAGATGATTCAAGATCGGCCCTTGCGTG 1002  
             || ||||| ||||| ||| | ||| ||||| ||| ||| ||| |  
SLR  : 955   AATTTCCGCATCAATGTTTGGGAAGGGGTAAAAGCCATGATCCGAGCCC GCCCTATCAT 1014  
  
ICTB : 1003  GGCATCGGCCCCCGGCAATAACCGCCTTTAAACCTGGTTTATCCCTCTATCAACAGCGCGC 1062  
             ||||| ||||| || ||||||||| ||||| ||||| ||| |||||  
SLR  : 1015  GGCATTGGCCCCAGGTAAACGAAGCCCTTTAACCAAATTTATCCTTACTATATGCGGCCCCGC 1074  
  
ICTB : 1063  TTTACGGCGTTGAGCGCCTACTCCGTCCTCCGCTGGAAAGTCGCGGTTGAGGGCGGACTACTG 1122  
             || || || ||||| ||||| ||||| || ||||| ||||| ||| |||  
SLR  : 1075  TTCACGGCCCTGAGTGCCTATTCCATTACCTAGAAATTTTGGTGGAACGGGTGTAGTT 1134  
  
ICTB : 1123  GGCTTGA-CGGCCTTCGCTTGGCTGCT-GCTGGTCACGGCGGTGACGGCGGTGCGGCAGG 1180  
             || || || || || ||||| ||||| || || || ||||| || |||  
SLR  : 1135  GGTTTTACCTGTATGCTC-TGGCTGTTGGCCGTTACCCTAGGCCAAGGC-GTAGAACTGG 1192  
  
ICTB : 1181  TGAGCCGACTGCGGCGCGGATCGCAATCCCC--AAGCCCTTTTGGTTGATGGCTAGCTTGGC 1238  
             | | ||||| || || || ||||| ||||| ||||| ||||| |||||  
SLR  : 1193  TTAAACG-CTGTGCGC-CAAACCCCTCGCCCCCGGAAGGCATCTGGATTATGGGGGCTTTAGC 1250  
  
ICTB : 1239  CGGTTTGGCAGGAATGCTGGGTCACGGTCTGTTTGATACCGTGCTCTATCGACCGGAAGC 1298  
             | | || ||||| ||||| ||||| ||||| ||||| ||||| |||  
SLR  : 1251  GCGGATCATCGGTTTGTGGTCCACGGCATGGTAGATACAGTCTGTGTACCGTCCCCCGGT 1310  
  
ICTB : 1299  CAGTACGCTCTGGTGGCTCTGTATTGG--AGCGATCGCGAGTTTCTGG--CAGC-CCCAA 1353  
             || || || ||||| || ||||| || ||||| || ||||| ||||| |||||  
SLR  : 1311  GAGCACTTTGTGGTGG-TTGCTAGTGGCCATTG-TTGCTAGTCAGTGGGCCAGCGGCCAG 1368  
  
ICTB : 1354  CCTTCCAAGCAACTCCCTCCAGAAGCCGAGCATTCAGACGAA 1395  
             | ||| || || ||||| ||||| ||||| ||||| |||||  
SLR  : 1369  GCCCGTTTGGAGGCCCAGTAAAGAA---GAAAAATGAGGACAAA 1407
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++W++L F + PQ+WG S LHRL G ++W +S L EALG L+A+++ +APF
SLR : 5 ISIWRSIMFGGSPQEWGRGSLHRLVGVGQSWIQASVLWPHFEALGTALVAIIFIAAPF 64

ICTB : 61 VPSSALGLGLAAIAYWALLSLTDIDLRQATPIHVLVLLYWGVDALATGLSPVRAAALVG 120
++ LG+ + A+WALL+ D + TPIH LV YW + A+A G SPV+ AA G

SLR : 65 TSTTMLGIFMLLCGAFWALLTFADQPGKGLTPIHVLVFAWYCISAIAGVGFSPVKMAASG 124

ICTB : 121 LAKLTLYLLVFALAAARVLRNPRRLRSLFSVVVITSLFVSVYGLNQWYGVVEELATWVDRN 180
LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + GVE+LATW D

SLR : 125 LAKLTANLCLFLLAARLLQNKQWLNRLVTVLLVGLLVGSYGLRQQVDGVEQLATWNDPT 184

ICTB : 181 SVADFTSRVYSYLGPNLAAAYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLILT 240
S +RVYS+LGPNLAAAYLVP T S +A+ VWR W PKLL + LCL T

SLR : 185 STLAQATRVYSFLGNPNLAAAYLVPMTGLSLSALVVWRWPKLLGATMVIVNLLCLFFT 244

ICTB : 241 YSRGGNLGFVAMIFVWALLGLYWFQPRLPAPWRRWLFPVVLGGLVAVLLVAVLGLEPLRV 300
SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+

SLR : 245 QSRGGWLAVALGATFLALCYFWWLPLQPKFWQRWSLPLAIAVAVILGGGALIAVEPIRL 304

ICTB : 301 RVLSIFVGREDSNNFRINVWLAVLQMIQDRPWLIGIGPGNTAFNLVYPLYQQARFTALSA 360
R +SIF GREDSNNFRINW V MI+ RP +GIGPGN AFN +YP Y + RFTALSA

SLR : 305 RAMSIFAGREDSNNFRINWEGVKAMIRARPIIGIGPGNEAFNQIYPYMRPRFTALSA 364

ICTB : 361 YSVPLEVAVEGGLGLTAFAWLLLVTAVTAVRQVSRRLRRDRNPQAFWLMAAGLMLG 420
YS+ LE+ VE G++G T WLL VT V V R R+ P+ W+M +LA + G+L

SLR : 365 YSIYLEILVETGVGFTCMLWLLAVTLGKGVELVKRCRQTLAPEGIWMGALAAIIGLLV 424

ICTB : 421 HGLEDTVLYRPEASTLWLCIGAIASFQWQPQPSKQLPPEAEHSDEKM 467
HG+ DTV YRP STLWWL + +AS W ++ + E+ D+ +

SLR : 425 HGMVDTVWYRPPVSTLWWLLVAIVASQWASQAARLEASKEENEDKPL 471

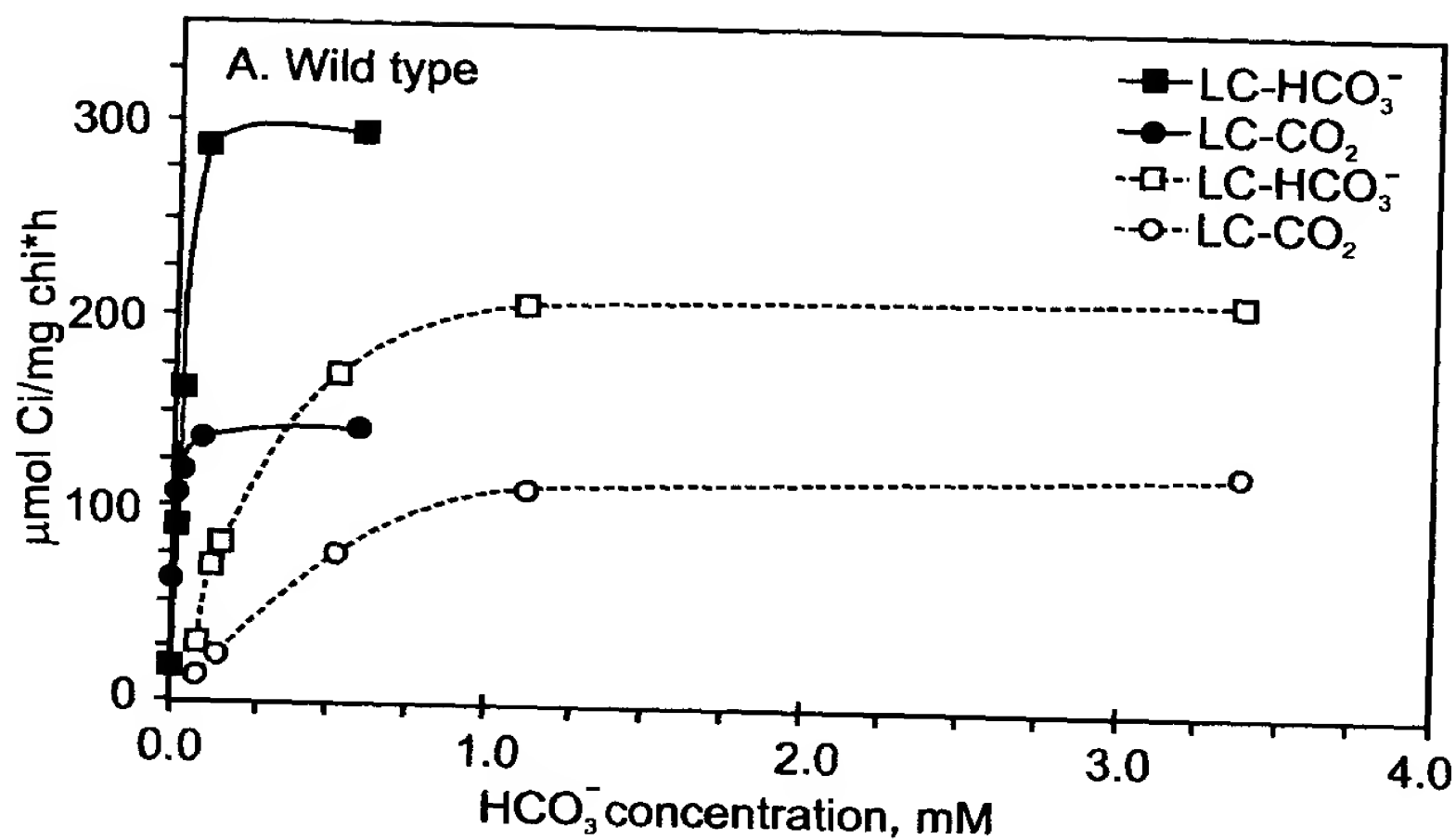


Fig. 4a

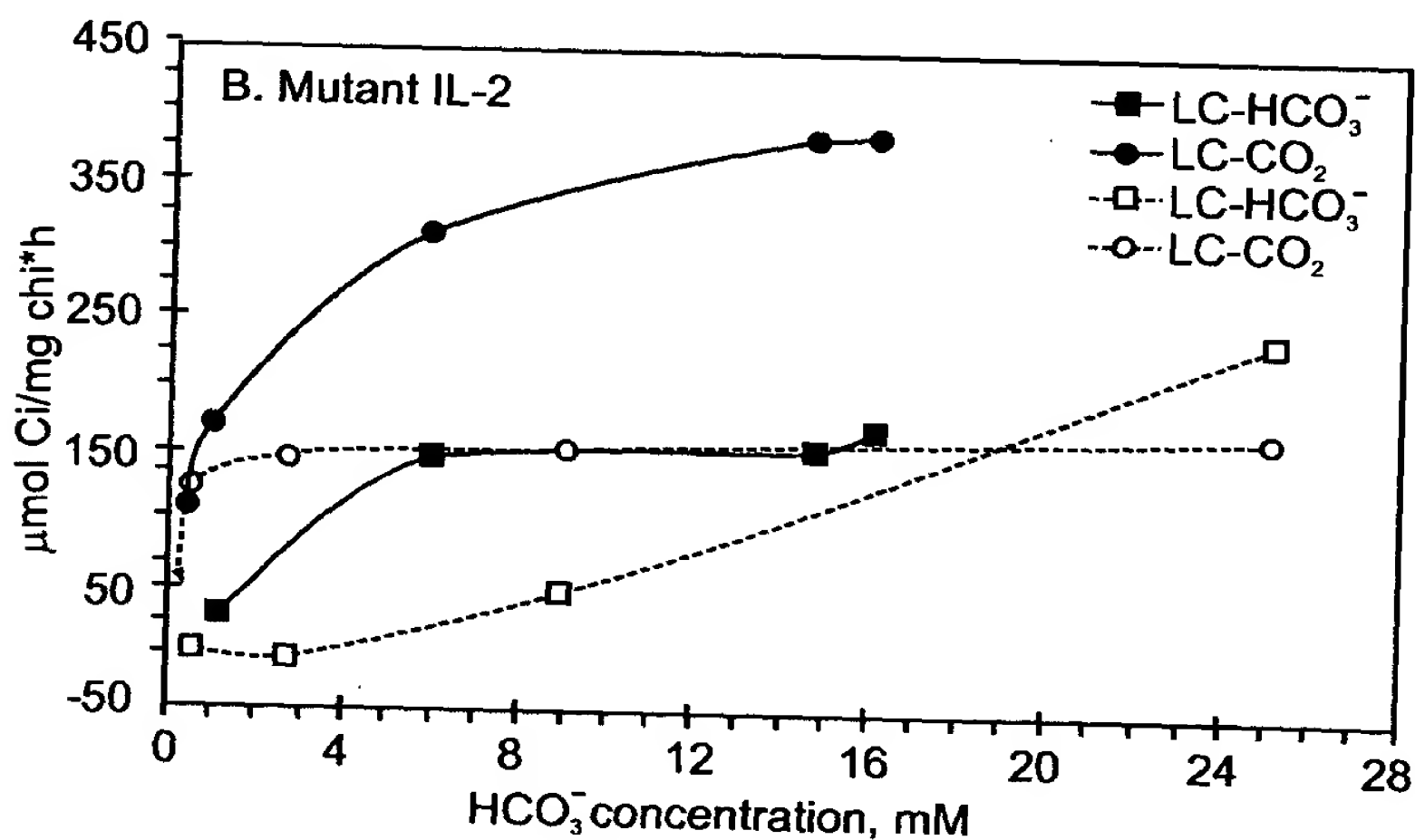


Fig. 4b



Wild type	GGGCT-AGCCGCGATCGCGGCTATTGGGCC	(SEQ ID NO: 6)
IL-2 ApaI side	GGGCT-AG--G-GATCGC-GCCTATTGGGCC	(SEQ ID NO: 7)
IL-2 BamHI side	GGGCTCA-----GATCGC-GCCTATTGGGCC	(SEQ ID NO: 8)
IctB	G L A A I A A Y W A L	(SEQ ID NO: 9)

Fig. 5

Transgenic
35S:ictB

WT A B C



Fig. 6

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